

Figure 1

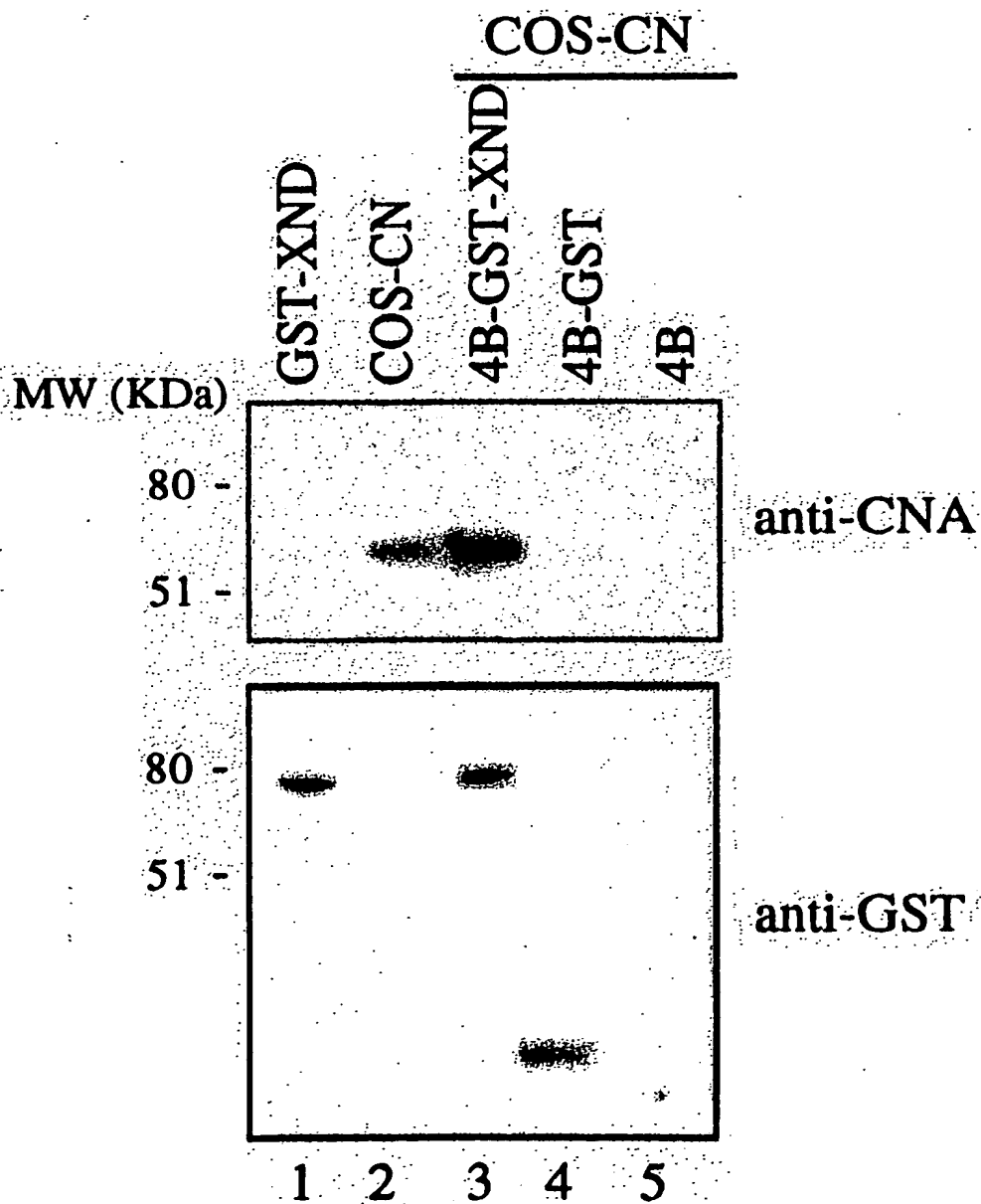


Figure 2

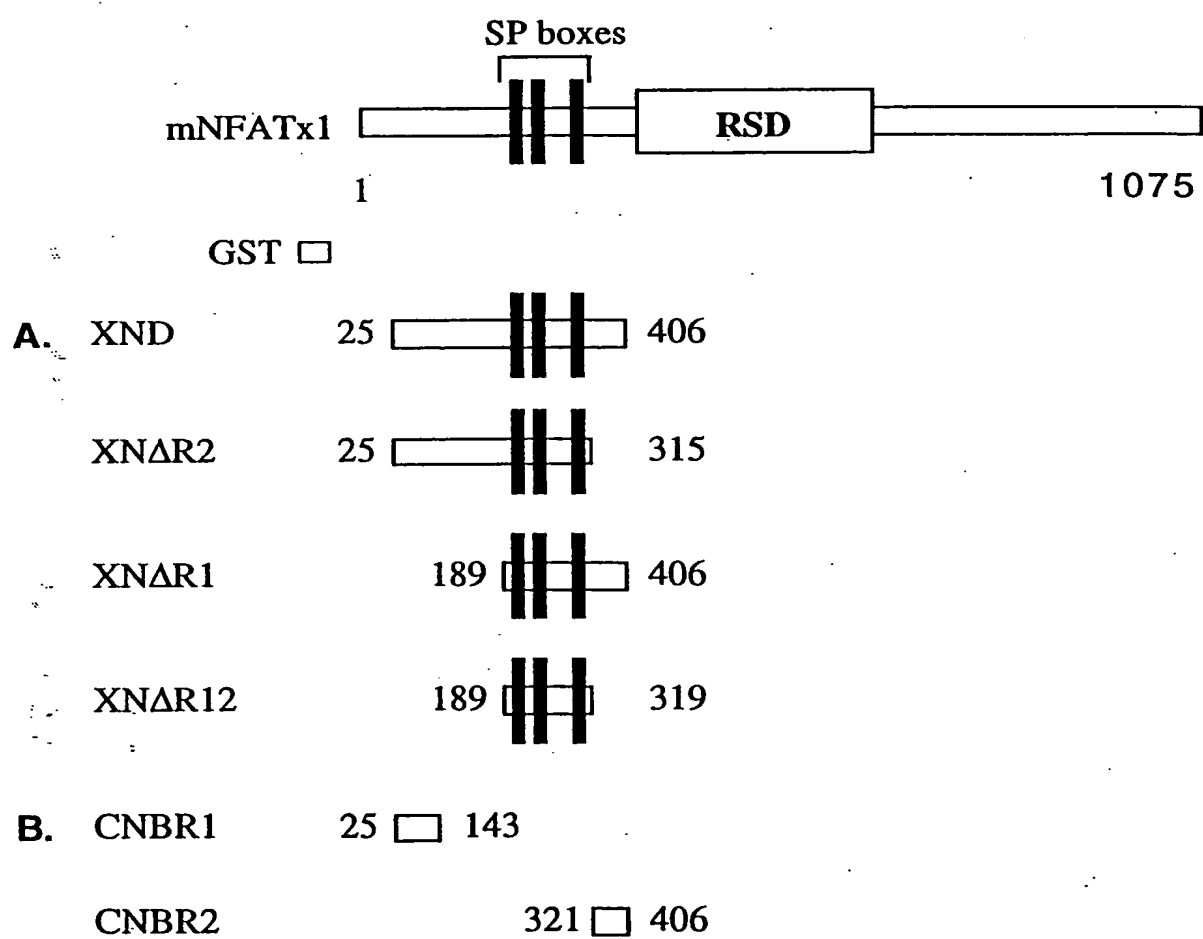


Figure 3

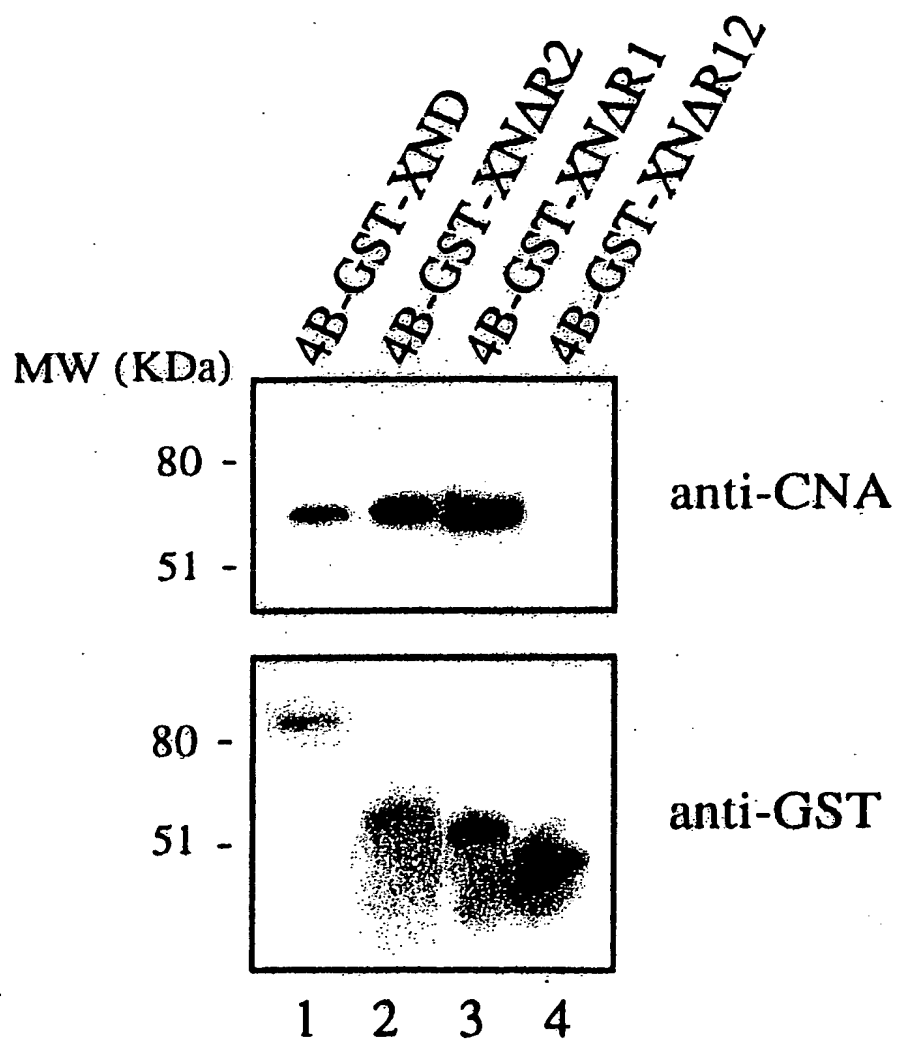


Figure 4

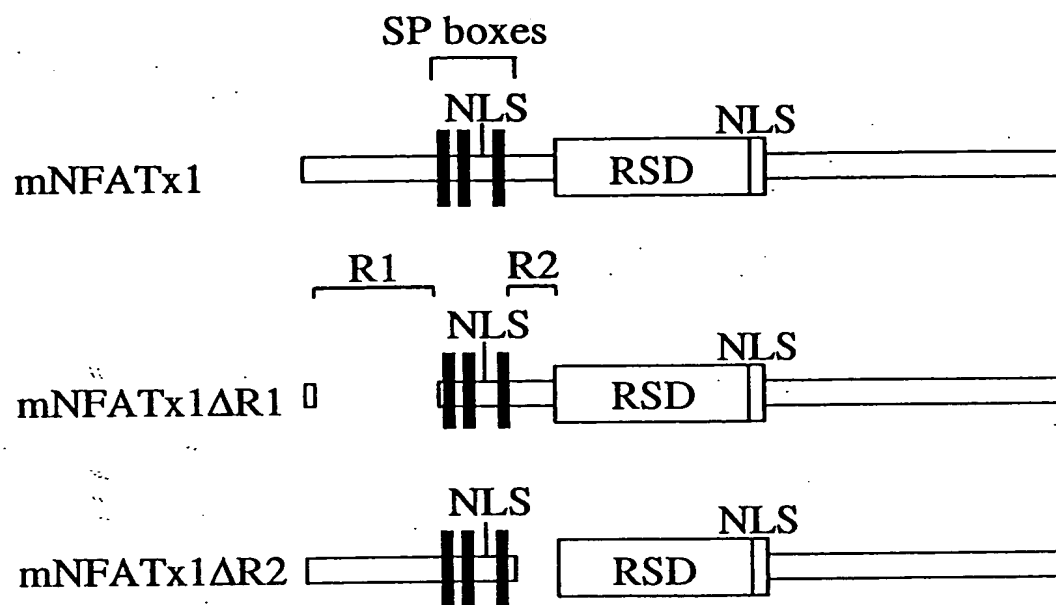


Figure 5

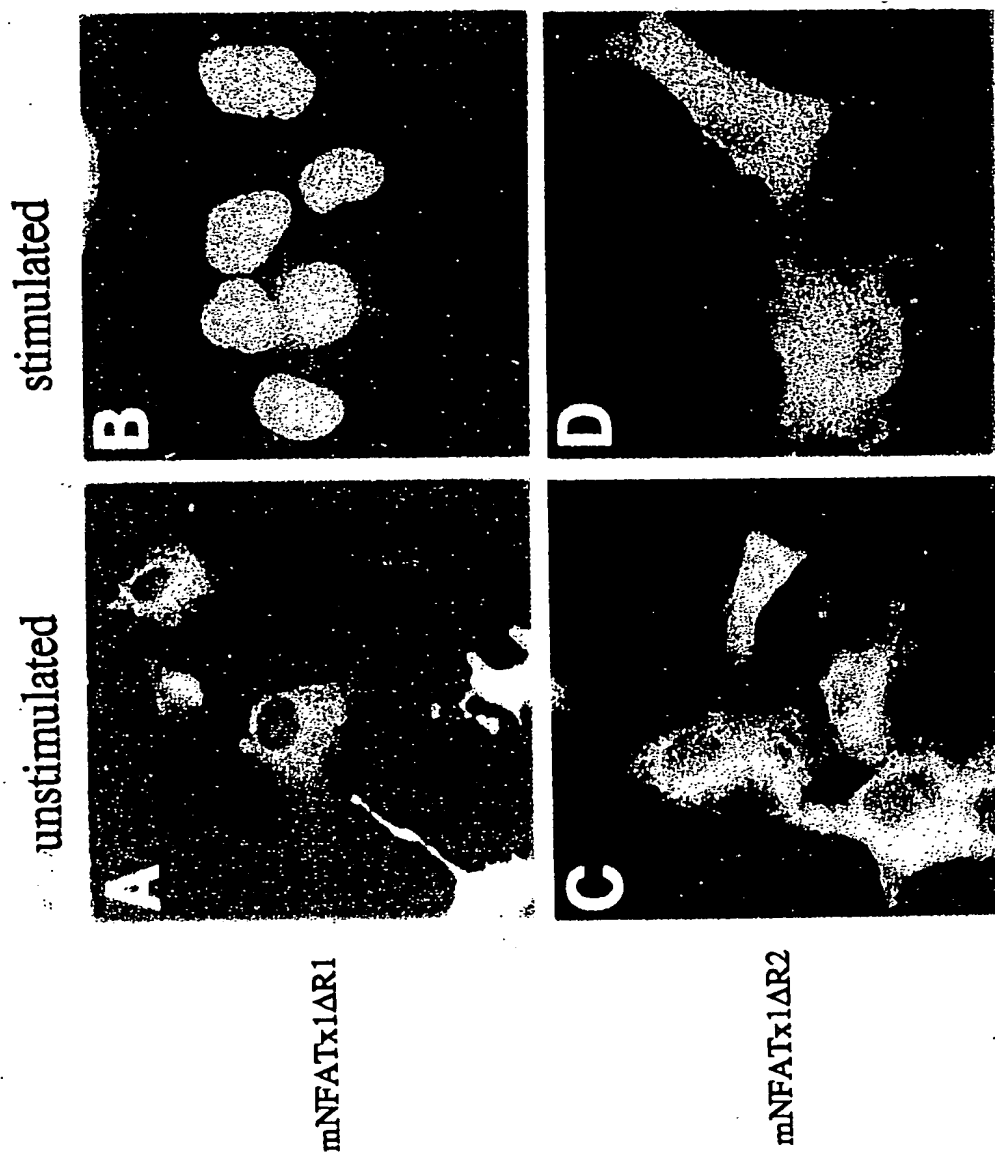


Figure 6

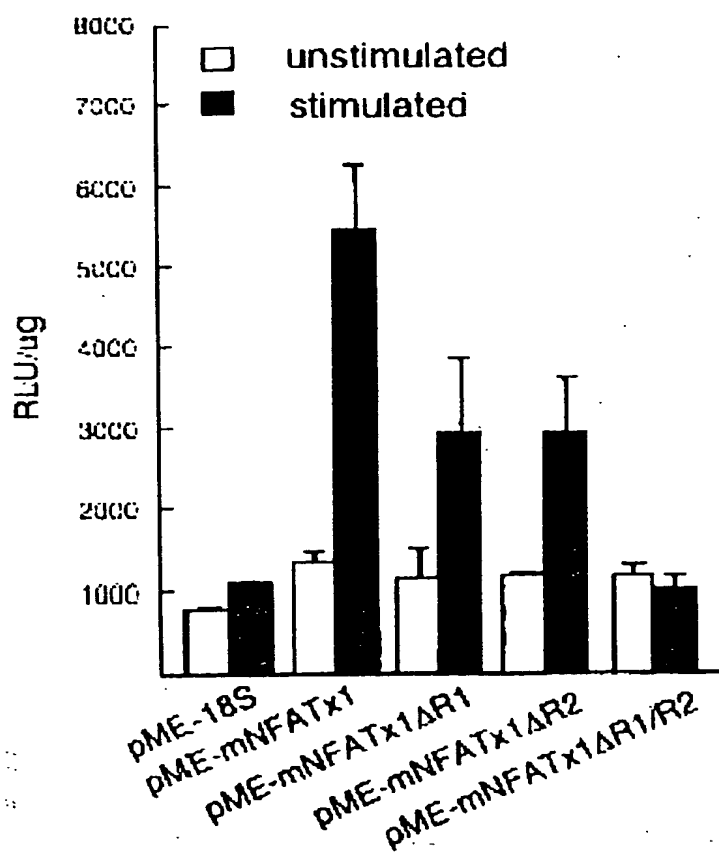
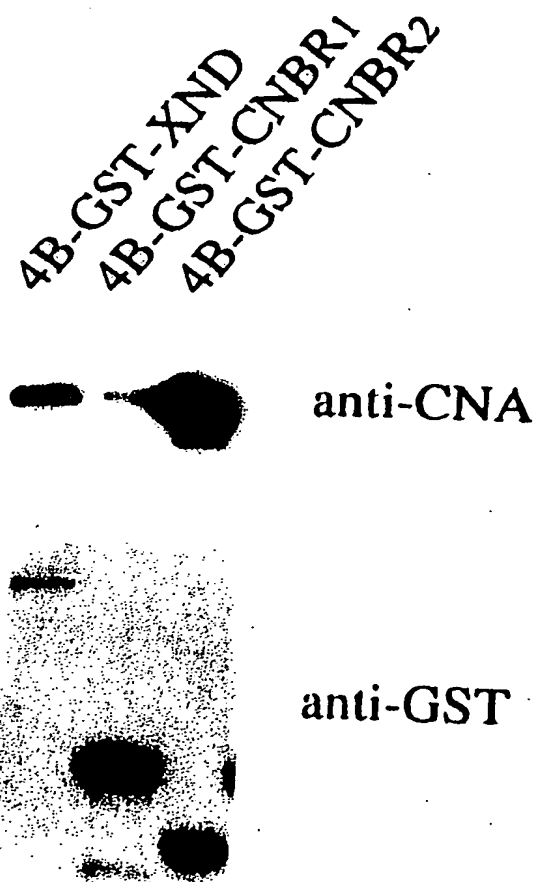


Figure 7



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Figure 8

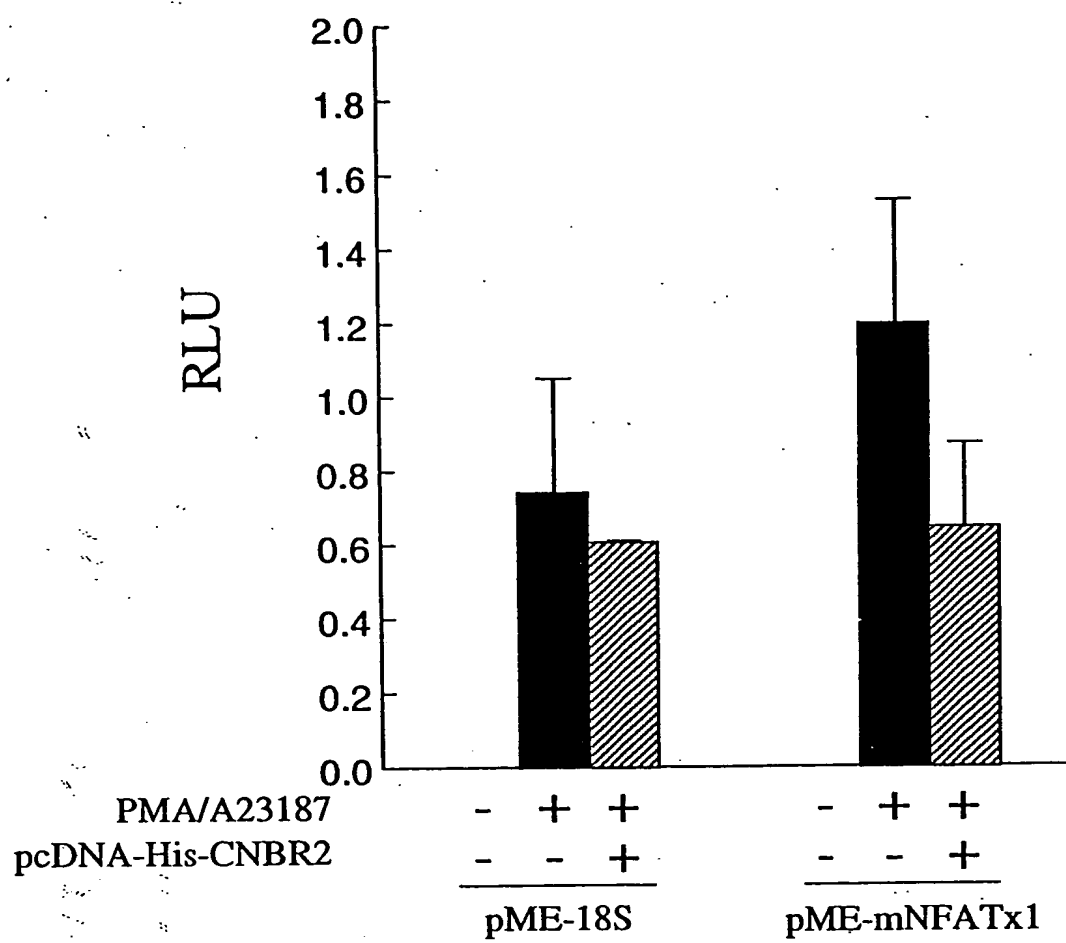


Figure 9

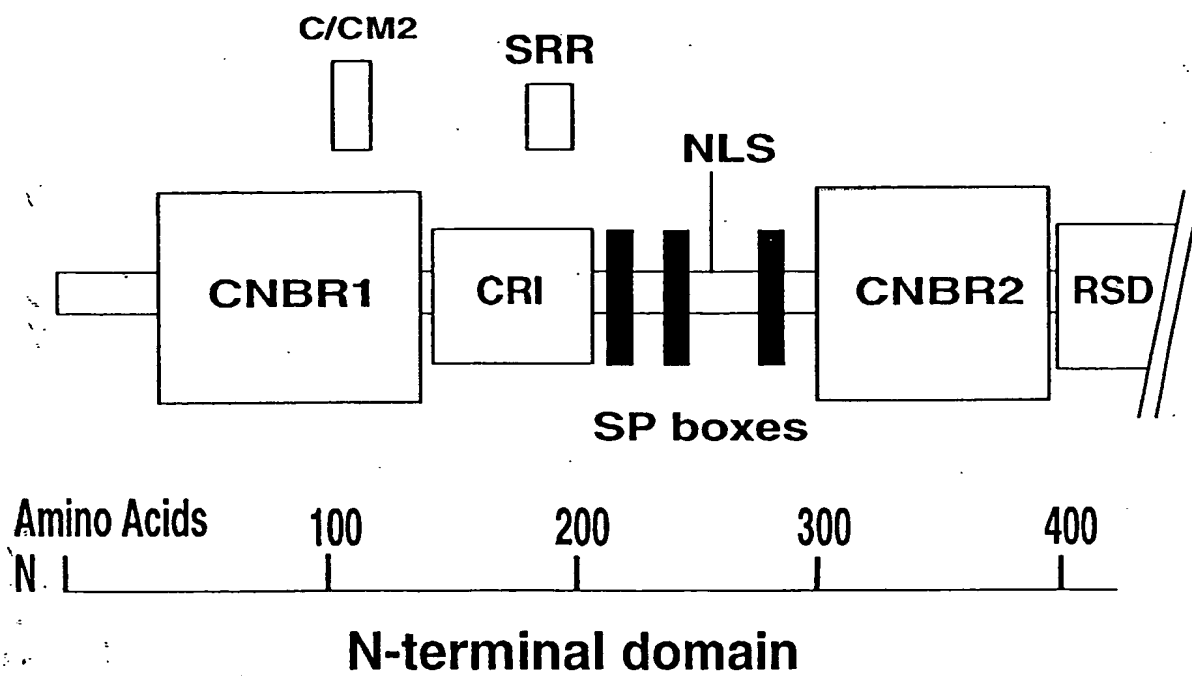


Figure 10

mNFATx	1	MTTANGAHDELDFKLVFGEDGAPAPPPGSRPADLEDDCASIIYFNVDPPSTLTTPCLPHHGL-PSHSSVLSPSFQ	79
hNFATx	1	79
NFATc3	1	PRRVLFVSVA QL.SRTR..PSDL.....NSS.G.....LQ.....	69
mNFATx	80	LQSHKNYEGTCEIPESKYSPLGGPKFECPSIQFTSISNCQQLDAHEDDLQINDPEREFLEPSRDHLYLPLEPSYRE	159
hNFATx	80I.....H.....	159
NFATc3	70	..GY.....GD.S.....I.....H.GT.....H.....Y.....	149
mNFATx	160	SSLSPASSISSRSWFSWFDASSCESLSHIYDDVDSELNEAAARFTLGSPLTSPGGSPGGCPGEESWHQYSGHSLSPRQ	239
hNFATx	160	239
NFATc3	150T.....L.....	229
mNFATx	240	SPCHSPRSSITDENWLSRPASGSSSRPTSPCGKRRRHSSAEVCYAGSLSPHSPVSPGHSRGSVTEDTWLTAPVHTGS	319
hNFATx	240V.....	319
NFATc3	230N.S..G.....	309
mNFATx	320	GLSPAPFPFYQCVETDIPLKTRKTSQAAAILPGKLEICSDQGNLSPSRETSDVDDGLGSQYPLKKDSSGDDFLSVPSPF	399
hNFATx	320	..G..V.....L.....S...A...I.....C.....	399
NFATc3	310	389
mNFATx	400	TWSKPKPGHTPIFRTSSLPLDWPLPTHFGQCELKIEVQPKTHRAHYETEGSRGAVKASTGGHPVVKLLGYSEKPINLQ	479
hNFATx	400A.....	479
NFATc3	390N.....	469
mNFATx	480	MFIGTADDRYLPHAFYQVHRITGKTIVATASQEIILIASTKVLEIPLPENNMASIDCAGILKLRNSDIELRKGETDIGR	559
hNFATx	480	479
NFATc3	470	469

Figure 11

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NFAT1L.....G.....E.....P.....	65
NFAT2	MNA PER QP QD GDA FGH EPG GSP QDE LDF S I L F D Y E L N P N E E E P N A H K V A S P S G P A Y P D D V M	64
NFAT3	MP S T S P V P S K F P L G P A A A V F G R G E T L G P A P R A G G T M K S A - E E H Y G Y A S S N V S P A L P L P T A H S T	59
	---M T T A N C C A H D E L D F K L V F G E D G A P A P P P G S R P A D L - - - E P D D C A S I Y I F N V D P P P S T L T T P	60
	---M G A A S C E D E L E F K L V F G E E K E A P P L G A G G L G E E L D - S E D A P P C C R L A L G E P P P Y G A A P I G	
NFAT1L.....G.....E.....P.....	122
NFAT2	DYGLK PYSPLAELSCEPPGRFRGEPDRVG-----PQKFLSAAKPAAGASGLSPRIEITPSHEL I	129
NFAT3	LPA PCHNLO TSTPG I I P P A D H P S G Y C A A L D G G P A G Y F L S G H T R P D G A P A L E S P R I E I T S C L G L Y	120
	LCLPHHGLPSSHSSVLSPSFQLQSHKNYEGT---CEIPESKYSPLGGPKPFECPSIQITSI SPNC	125
	I P R P P P R P C M H S P P P R P A P S P G T W E S Q P A R S V R L G G P G G A C G A G G R V L E C P S I R I T S I S P T P	
NFAT1V.....YRE.....SSLSS.S.	178
NFAT2	QAVGPLRMRDAGLLVEQPLLAGVAA SPRFTLPVPGFEGYRE-----PLCLSPASSGSSASF	182
NFAT3	HNNNQFPH---DVEVEDVLPSSKRS PSTAATLSLPLEAYRD-----PCLSPASSLSRSC	175
	HQELDAHE---DDLQINDPEREFLEPSPRDHLYLPLEPSYRES-----SLSPSPASSISRSW	181
	EPPAA-----LEONPDANWDCGSPRDYPPFEFGCGYREAGACGGGAFPPSPSPGSSLSRWSF	
NFAT1L.....E.....	216
NFAT2	ISDT-----PSPYTPSPCVSPNNGGPD D L C P O F O N I P A H - Y S P R T	216
NFAT3	NSEASSYESNY-----SYPYASPQTSPWQSPCVSPKTTDPEEGFPRGLGACTLLCSPQH	239
	PSDASCELSH IYODVDSELNEAAARETLGSPLTSPGGSPGCGPGEETWHQOYGLGHS-LSPRO	235
	PSDASDEAALYAACDEVESELNEAASRFCLGSPLPSPRA SPRPWT PEDPWSLY-----	
NFAT1L.....R.....SP...KRR.S.....SP...S	280
NFAT2	SPIHSPRTSLAEDSCLGRHS-PVPRPASRRSSSPGAKRRHS CAEALVALPPGASPOQRSRSPSPQPS	290
NFAT3	SPSTSPRASVTEESWLG-----ARSSRPASPCNKRYSLNGR---QPPYSPHSHSPTPSPHGS	300
	SPCHSPSSVTDENMLSPRP-ASGPPSSRPTSPCGKRRHSSAEVC---YAGSLSPHSHSPVSPCHS	285
	--GPSPGCRGPEDSWLLLSAPGPTPASPRPASPCGKPPYSS-----SGTPSRA SPALS	
NFAT1L.....IP.K.KTS.D.....	342
NFAT2	SHVAPQDHGSPAGYPPVAGSAVIM---DALNSLATDSPCGIPPRMMWKTSPDPSPVSAAPS KAGLP	355
NFAT3	PRVSVTDDSWLGNNTQYTSSAIVAAINALTTDSSLDLGDGVVKNRKTLEGGPSVALKVEPVGE	360
	PRGSVTEDTLNASHVHGSGGLGP---AVFPYQYCVETDIPLKTTRKTSBDQAAI LPGKLELCS	350
	RGSLGEEGSEPPPPPLPLARDPGSPGPFYVCGAPAESIPQKTRRTSSEDAVALPRSEEPASC	
NFAT1A.....L.VP.....W.K.....T..LP	395
NFAT2	RHIYP-----AVEFLGPCCEQGERRNSAPESILLVP---PTWPKPLVPAIPICSI PVTASLP	413
NFAT3	DUGSPFP-PADPAPEDYSSFCIRKCGFCDOYLAVPOHPYQAKPKP---LSPTSYMSPTLP	418
	DQGLSPARETSIDDLGSLQYPLKDDSCGDFLSVPS-PFTUSKPKP---GHTPIFRTSLP	404
	NCKLP-----LGAEESVAPP CGSPKEVAGMDYLA VPS-CLAUSKARIQ---GHSPIFRTSALP	